RAW SEQUENCE LISTING
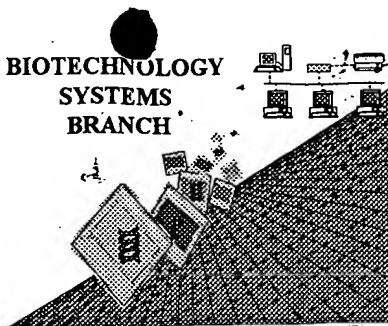# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/910,358_

Source: _OIPE_

Date Processed by STIC: _8/1/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
 PATENTIN 2.1 e-mail help: patin21help@uspto.gov **or phone 703-306-4119 (R. Wax)**
 PATENTIN 3.0 e-mail help: patin3help@uspto.gov **or phone 703-306-4119 (R. Wax)**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED   **SUGGESTED CORRECTION**   **SERIAL NUMBER:** 09/910,358

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length

Sequence(s)_____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)	SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

```
        RAW SEQUENCE LISTING                    DATE: 08/01/2001
        PATENT APPLICATION:  US/09/910,358      TIME: 11:05:11

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        Output Set: N:\CRF3\08012001\I910358.raw
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Does Not Comply
Corrected Diskette Needed

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 3 <110> APPLICANT: Shi, Wenyuan
 4         Anderson, Maxwell
 5         Morrison, Sherie
 6         Trinh, Kham
 7         Wims, Letitia
 8         Chen, Li
10 <120> TITLE OF INVENTION: Fusion Proteins for Targeted Delivery of Antimicrobial
Peptides
12 <130> FILE REFERENCE: 22851-033
14 <140> CURRENT APPLICATION NUMBER: US/09/910,358
14 <141> CURRENT FILING DATE: 2001-07-19
14 <150> PRIOR APPLICATION NUMBER: US 09/378,577
15 <151> PRIOR FILING DATE: 1999-08-20
17 <160> NUMBER OF SEQ ID NOS: 15
19 <170> SOFTWARE: PatentIn version 3.1
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22 <211> LENGTH: 563
23 <212> TYPE: DNA
24 <213> ORGANISM: Synthetic-Murine
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28 <222> LOCATION: (69)..(140)
29 <223> OTHER INFORMATION: Histatin 5
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (141)..(188)
35 <223> OTHER INFORMATION: Linker Peptide
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39 <221> NAME/KEY: CDS
40 <222> LOCATION: (189)..(563)
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48          Asp Ser His Ala Lys Arg His His Gly Tyr Lys Arg Lys Phe
49           1               5                  10
51 cac gag aag cac cac tcg cac aga gga tac tct ggt ggc ggt ggc tcg      158
52 His Glu Lys His His Ser His Arg Gly Tyr Ser Gly Gly Gly Gly Ser
53 15                  20                  25                  30
55 ggc gga ggt ggg tcg ggt ggc ggc gga tcc gac gtg aag ctt gtg gag      206
56 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Lys Leu Val Glu
57                     35                  40                  45
59 tct ggg gga ggc tta gtg aac cct gga ggg tcc ctg aaa ctc tcc tgt      254
60 Ser Gly Gly Gly Leu Val Asn Pro Gly Gly Ser Leu Lys Leu Ser Cys
61                 50                  55                  60
63 gca gcc tct gga ttc act ttc agt agc tat acc atg tct tgg gtt cgc      302
64 Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg
65              65                  70                  75
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invalid - see item 10 on Error Summary sheet

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67 cag act ccg gag aag agg ctg gag tgg gtc gca tcc att agt agt ggt     350
68 Gln Thr Pro Glu Lys Arg Leu Glu Trp Val Ala Ser Ile Ser Ser Gly
69     80                  85                  90
71 ggt act tac acc tac tat cca gac agt gtg aag ggc cga ttc acc atc     398
72 Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile
73 95                 100                 105                 110
75 tcc aga gac aat gcc aag aac acc ctg tac ctg caa atg acc agt ctg     446
76 Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln Met Thr Ser Leu
77             115                 120                 125
79 aag tct gag gac aca gcc atg tat tac tgt tca aga gat gac ggc tcc     494
80 Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ser Arg Asp Asp Gly Ser
81             130                 135                 140
83 tac ggc tcc tat tac tat gct atg gac tac tgg ggt caa gga acc tca     542
84 Tyr Gly Ser Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
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108 <211> LENGTH: 16
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134             35                  40                  45
137 Ala Ser Ile Ser Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val
138     50                  55                  60
141 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
142 65                  70                  75                  80
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170 <222> LOCATION: (111)..(158)
171 <223> OTHER INFORMATION: Linker Peptide
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184          Lys Arg Leu Phe Lys Glu Leu Lys Phe Ser Leu Arg Lys Tyr
185          1               5.                      10
187 tct ggt ggc ggt ggc tcg ggc gga ggt ggg tcg ggt ggc ggc gga tcc     158
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189 15                  20                  25                  30
191 gac gtg aag ctt gtg gag tct ggg gga ggc tta gtg aac cct gga ggg     206
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193             35                  40                  45
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197         50                  55                  60
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201         65                  70                  75
203 gca tcc att agt agt ggt ggt act tac acc tac tat cca gac agt gtg     350
204 Ala Ser Ile Ser Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val
205     80                  85                  90
207 aag ggc cga ttc acc atc tcc aga gac aat gcc aag aac acc ctg tac     398
208 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
209 95                  100                 105                 110
211 ctg caa atg acc agt ctg aag tct gag gac aca gcc atg tat tac tgt     446
212 Leu Gln Met Thr Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
213             115                 120                 125
215 tca aga gat gac ggc tcc tac ggc tcc tat tac tat gct atg gac tac     494
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217             130                 135                 140
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262             35                  40                  45
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266     50                  55                  60
269 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
270 65                  70                  75                  80
273 Leu Gln Met Thr Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
274             85                  90                  95
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VERIFICATION SUMMARY   DATE: 08/01/2001
PATENT APPLICATION: **US/09/910,358**   TIME: 11:05:12

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Output Set: **N:\CRF3\08012001\I910358.raw**

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date